

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/768, 886 B  
Source: IFW/6  
Date Processed by STIC: 06/21/2006

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 06/21/2006

PATENT APPLICATION: US/10/768,886B

TIME: 15:18:17

Input Set : A:\MAPK5 (Supp).txt

Output Set: N:\CRF4\06212006\J768886B.raw

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3 <110> APPLICANT: Board of Trustees for University of Arkansas
5 <120> TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to
Enhance
6     Biotic and Abiotic Stress Tolerance in Plants
8 <130> FILE REFERENCE: UAF-03-14
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/768,886B
11 <141> CURRENT FILING DATE: 2004-01-31
13 <160> NUMBER OF SEQ ID NOS: 10
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1396
19 <212> TYPE: DNA
20 <213> ORGANISM: Oryza sativa
22 <400> SEQUENCE: 1
23 agagagtcag ataagggtcgt taattaggtt ggtcaattcg gctgcttgcg gcgagagaag      60
25 aggaggaggg attagggatg gacggggcgc cgggtggcgga gttcaggccg acgatgacgc      120
27 acggcggccg gtacctgctc tacgacatct tcgggaacaa gttcgagggtg acgaacaagt      180
29 accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgctctgc tccgtgatga      240
31 acttttgagac gaggggagatg gtggcgcataa agaagatcgc caacgcggtt aacaacgaca      300
33 tggacgccaa gcgcacgctc cgggagatca agctcctcag gcacctcgac cagcagaaca      360
35 tcataggcat cagggatgtg atcccgccgc cgatccctca ggcgttcaac gacgtctaca      420
37 tcgccacgga gctcatggac accgacctcc atcacatcat ccgctccaac caagaactgt      480
39 cagaagagca ctgccagtat ttcctgtacc agatcctgcg ggggctcaag tacatccact      540
41 cggcgaacgt gatccaccgc gacctgaagc cgagcaacct gctgctgaac gccaaactgcg      600
43 acctcaagat ctgcgaactt cggctggcgc ggccgctcgtc ggagagcgac atgatgacgg      660
45 agtacgtggg caccgggtgg taccgcgcgc cggagctgct gctcaactcc accgactact      720
47 ccgccgccat cgacgtctgg tccgtcggct gcatcttcat ggagctcatc aaccgccagc      780
49 cgctcttccc cggcaggggac cacatgcacc agatgcgcct catcaccgag gtgatcgga      840
51 cgccgacgga cgacgagctg gggttcatac ggaacgagga cgcgaggaag tacatgaggc      900
53 acctgccgca gtacccgcgc cggacgttcg cgagcatggt cccgcgggtg cagccccgccg      960
55 cgctcgacct catcgagagg atgctcacct tcaaccgcgt gcagagaatc acagttgagg      1020
57 aggcgctcga tcacctttac ctagagagat tgcacgacat cgccgatgag cccatctgcc      1080
59 tggagccctt ctcttcgac ttcgagcaga aggctctaaa cgaggaccaa atgaagcagc      1140
61 tgatcttcaa cgaagcgatc gagatgaacc caaacatccg gtactagatt gaatcaccat      1200
63 ggaaatgaga tcccgctctat acctgctttg tacatatgat caagattgag agccgggtag      1260
65 actgaacatt gcatttgttt gtttgttgat gttcgaaacc cacattctct gcaagttgtg      1320
67 gctgctttgt atgatatatg gtactatggt cgaataaaaag ggtttggaac tttggattaa      1380
69 aaaaaaaaaa aaaaaa
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 368
74 <212> TYPE: PRT
75 <213> ORGANISM: Oryza sativa
77 <400> SEQUENCE: 2
79 Met Asp Gly Ala Pro Val Ala Glu Phe Arg Pro Thr Met Thr His Gly

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80 1          5          10          15
83 Gly Arg Tyr Leu Leu Tyr Asp Ile Phe Gly Asn Lys Phe Glu Val Thr
84          20          25          30
87 Asn Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Arg Gly Ala Tyr Gly
88          35          40          45
91 Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala Ile
92          50          55          60
95 Lys Lys Ile Ala Asn Ala Phe Asn Asn Asp Met Asp Ala Lys Arg Thr
96 65          70          75          80
99 Leu Arg Glu Ile Lys Leu Leu Arg His Leu Asp His Glu Asn Ile Ile
100          85          90          95
103 Gly Ile Arg Asp Val Ile Pro Pro Pro Ile Pro Gln Ala Phe Asn Asp
104          100          105          110
107 Val Tyr Ile Ala Thr Glu Leu Met Asp Thr Asp Leu His His Ile Ile
108          115          120          125
111 Arg Ser Asn Gln Glu Leu Ser Glu Glu His Cys Gln Tyr Phe Leu Tyr
112          130          135          140
115 Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Ile His
116 145          150          155          160
119 Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Ala Asn Cys Asp Leu
120          165          170          175
123 Lys Ile Cys Asp Phe Gly Leu Ala Arg Pro Ser Ser Glu Ser Asp Met
124          180          185          190
127 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
128          195          200          205
131 Leu Asn Ser Thr Asp Tyr Ser Ala Ala Asp Val Trp Ser Val Gly Cys
132          210          215          220
135 Ile Phe Met Glu Leu Ile Asn Arg Gln Pro Leu Phe Pro Gly Arg Asp
136 225          230          235          240
139 His Met His Gln Met Arg Leu Ile Thr Glu Val Ile Gly Thr Pro Thr
140          245          250          255
143 Asp Asp Glu Leu Gly Phe Ile Arg Asn Glu Asp Ala Arg Lys Tyr Met
144          260          265          270
147 Arg His Leu Pro Gln Tyr Pro Arg Arg Thr Phe Ala Ser Met Phe Pro
148          275          280          285
151 Arg Val Gln Pro Ala Ala Leu Asp Leu Ile Glu Arg Met Leu Thr Phe
152          290          295          300
155 Asn Pro Leu Gln Arg Ile Thr Val Glu Glu Ala Leu Asp His Pro Tyr
156 305          310          315          320
159 Leu Glu Arg Leu His Asp Ile Ala Asp Glu Pro Ile Cys Leu Glu Pro
160          325          330          335
163 Phe Ser Phe Asp Phe Glu Gln Lys Ala Leu Asn Glu Asp Gln Met Lys
164          340          345          350
167 Gln Leu Ile Phe Asn Glu Ala Ile Glu Met Asn Pro Asn Ile Arg Tyr
168          355          360          365
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 1084
173 <212> TYPE: DNA
174 <213> ORGANISM: Oryza sativa

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176 <400> SEQUENCE: 3
177 agagagtcag ataaggtcgt taattagggtt ggtcaattcg gctgcttgcg gcgagagaag      60
179 aggaggaggg attagggatg gacggggcgc cggtggcgga gttcaggccg acgatgacgc      120
181 acggcgcccg gtacctgctc tacgacatct tcgggaacaa gttcgagggtg acgaacaagt      180
183 accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtgatga      240
185 actttgagac gagggagatg gtggcgataa agaagatcgc caactgcgac ctcaagatct      300
187 gcgacttcgg gctggcgcgg ccgtcgtcgg agagcgacat gatgacggag tacgtggtca      360
189 cccggtggta ccgcgcgccg gagctgctgc tcaactccac cgactactcc gccgccatcg      420
191 acgtctggtc cgtcggctgc atcttcatgg agctcatcaa ccgccagccg ctcttccccg      480
193 gcagggacca catgcaccag atgcgcctca tcaccgaggt gatcgggacg ccgacggacg      540
195 acgagctggg gttcatacgg aacgaggacg cgaggaagta catgaggcac ctgccgcagt      600
197 acccgcgccg gacgttcgcg agcatgttcc cgcgggtgca gcccgcgcg ctcgacctca      660
199 tcgagaggat gctcaccttc aacccgctgc agagaatcac agttgaggag gcgctcgatc      720
201 atccttacct agagagattg cacgacatcg ccgatgagcc catctgcctg gagcccttct      780
203 ccttcgactt cgagcagaag gctctaaacg aggacaaat gaagcagctg atcttcaacg      840
205 aagcgatcga gatgaaccca aacatccggt actagattga atcaccatgg aaatgagatc      900
207 ccgtctatac ctgctttgta catatgatca agattgagag ccgggtagac tgaacattgc      960
209 atttgtttgt ttgttgatgt tcgaaaccca cattctctgc aagttgtggc tgctttgtat     1020
211 gatatatggt actatgttcg aataaaaggg tttggaactt tggattaaaa aaaaaaaaaa     1080
213 aaaa                                                                1084
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 266
218 <212> TYPE: PRT
219 <213> ORGANISM: Oryza sativa
221 <400> SEQUENCE: 4
223 Met Met Asp Gly Ala Pro Val Ala Glu Phe Arg Pro Thr Met Thr His
224 1          5          10          15
227 Gly Gly Arg Tyr Leu Leu Tyr Asp Ile Phe Gly Asn Lys Phe Glu Val
228          20          25          30
231 Thr Asn Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Arg Gly Ala Tyr
232          35          40          45
235 Gly Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala
236          50          55          60
239 Ile Lys Lys Ile Ala Asn Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu
240 65          70          75          80
243 Ala Arg Pro Ser Ser Glu Ser Asp Met Met Thr Glu Tyr Val Val Thr
244          85          90          95
247 Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Asn Ser Thr Asp Tyr Ser
248          100         105         110
251 Ala Ala Ile Asp Val Trp Ser Val Gly Cys Ile Phe Met Glu Leu Ile
252          115         120         125
255 Asn Arg Gln Pro Leu Phe Pro Gly Arg Asp His Met His Gln Met Arg
256          130         135         140
259 Leu Ile Thr Glu Val Ile Gly Thr Pro Thr Asp Asp Glu Leu Gly Phe
260 145         150         155         160
263 Ile Arg Asn Glu Asp Ala Arg Lys Tyr Met Arg His Leu Pro Gln Tyr
264          165         170         175
267 Pro Arg Arg Thr Phe Ala Ser Met Phe Pro Arg Val Gln Pro Ala Ala
268          180         185         190

```

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```

271 Leu Asp Leu Ile Glu Arg Met Leu Thr Phe Asn Pro Leu Gln Arg Ile
272      195                      200                      205
275 Thr Val Glu Glu Ala Leu Asp His Pro Tyr Leu Glu Arg Leu His Asp
276      210                      215                      220
279 Ile Ala Asp Glu Pro Ile Cys Leu Glu Pro Phe Ser Phe Asp Phe Glu
280 225                      230                      235                      240
283 Gln Lys Ala Leu Asn Glu Asp Gln Met Lys Gln Leu Ile Phe Asn Glu
284      245                      250                      255
287 Ala Ile Glu Met Asn Pro Asn Ile Arg Tyr
288      260                      265
291 <210> SEQ ID NO: 5
292 <211> LENGTH: 26
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial
296 <220> FEATURE:
297 <223> OTHER INFORMATION: gene-specific primer containing restriction site
299 <400> SEQUENCE: 5
300 cgggatccgt cggctgcatc ttcatg                                     26
303 <210> SEQ ID NO: 6
304 <211> LENGTH: 25
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial
308 <220> FEATURE:
309 <223> OTHER INFORMATION: gene-specific primer containing restriction site
311 <400> SEQUENCE: 6
312 gctctagatt caatctagta ccgga                                     25
315 <210> SEQ ID NO: 7
316 <211> LENGTH: 20
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial
320 <220> FEATURE:
321 <223> OTHER INFORMATION: gene-specific primer containing restriction site
323 <400> SEQUENCE: 7
324 gagttcaggc cgacgatgac                                         20
327 <210> SEQ ID NO: 8
328 <211> LENGTH: 20
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial
332 <220> FEATURE:
333 <223> OTHER INFORMATION: gene-specific primer containing restriction site
335 <400> SEQUENCE: 8
336 atcggcgatg tcgtgcaatc                                         20
339 <210> SEQ ID NO: 9
340 <211> LENGTH: 368
341 <212> TYPE: PRT
342 <213> ORGANISM: Triticum aestivum
344 <400> SEQUENCE: 9
346 Met Asp Gly Ala Pro Val Ala Glu Phe Arg Pro Thr Met Thr His Gly
347 1                      5                      10                      15

```

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```

350 Gly Arg Phe Leu Leu Tyr Asn Ile Phe Gly Asn Gln Phe Glu Thr Thr
351          20          25          30
354 Ala Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Lys Gly Ala Tyr Gly
355          35          40          45
358 Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala Ser
359          50          55          60
362 Lys Lys Ile Ala Asn Ala Phe Asp Asn Asn Met Asp Ala Lys Arg Thr
363 65          70          75          80
366 Leu Arg Glu Ile Lys Leu Leu Leu Arg His Leu Asp Glu Asn Ile Val
367          85          90          95
370 Gly Leu Arg Asp Val Ile Pro Pro Ala Ile Pro Gln Ser Glu Asn Asp
371          100         105         110
374 Val Tyr Ile Ala Thr Glu Leu Met Asp Thr Asp Leu His His Ile Ile
375          115         120         125
378 Arg Ser Asn Gly Glu Leu Ser Glu Glu His Glu Gln Tyr Phe Leu Tyr
379          130         135         140
382 Gln Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Ile His
383 145         150         155         160
386 Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Ala Asn Cys Asp Leu
387          165         170         175
390 Lys Ile Cys Asp Phe Gly Leu Ala Arg Pro Ser Ser Glu Ser Asp Met
391          180         185         190
394 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
395          195         200         205
398 Leu Asn Ser Thr Asp Tyr Ser Ala Asn Ile Asp Val Trp Ser Val Gly
399          210         215         220
402 Cys Ile Phe Met Glu Leu Ile Asn Arg Ala Pro Leu Phe Pro Gly Arg
403 225         230         235         240
406 Asp His Met His Gln Met Arg Leu Ile Thr Glu Val Ile Gly Thr Pro
407          245         250         255
410 Thr Asp Asp Asp Leu Gly Phe Ile Arg Asn Glu Asp Ala Arg Arg Tyr
411          260         265         270
414 Met Arg His Leu Pro Gln Phe Pro Arg Arg Ser Phe Pro Gly Phe Pro
415          275         280         285
418 Lys Val Gln Pro Ala Ala Leu Asp Leu Ile Glu Arg Met Leu Thr Phe
419          290         295         300
422 Asn Pro Leu Gln Arg Ile Thr Val Glu Glu Ala Leu Glu His Pro Tyr
423 305         310         315         320
426 Leu Glu Arg Leu His Asp Val Ala Asp Glu Pro Ile Cys Thr Asp Pro
427          325         330         335
430 Phe Ser Phe Asp Phe Glu Gln His Pro Leu Thr Glu Asp Gln Met Lys
431          340         345         350
434 Leu Ile Pro Glu Asn Glu Ala Leu Glu Leu Asn Pro Asn Phe Arg Tyr
435          355         360         365
438 <210> SEQ ID NO: 10
439 <211> LENGTH: 371
440 <212> TYPE: PRT
441 <213> ORGANISM: Nicotiana tabacum
443 <400> SEQUENCE: 10

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/768,886B

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8

**VERIFICATION SUMMARY**

PATENT APPLICATION: **US/10/768,886B**

DATE: 06/21/2006

TIME: 15:18:19

Input Set : **A:\MAPK5 (Supp).txt**

Output Set: **N:\CRF4\06212006\J768886B.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number